

>IPI00083978.2 ACCESSION:IPI00083978 NID: Homo sapiens (Human).
SIMILAR TO CD63 PROTEIN. IPI_human
Length = 220

Score = 456 bits (1160), Expect = e-127
Identities = 216/216 (100%), Positives = 216/216 (100%)

Query: 33 AWLLLDNRNNFLTAFDENNHFFIVPISQILIGMGSSTVLFCLLGYIGIHNEIRWLLIVYAV
AWLLLDNRNNFLTAFDENNHFFIVPISQILIGMGSSTVLFCLLGYIGIHNEIRWLLIVYAV
Sbjct: 5 AWLLLDNRNNFLTAFDENNHFFIVPISQILIGMGSSTVLFCLLGYIGIHNEIRWLLIVYAV

Query: 93 ITWTFAVQVVLSAFIITKKEEVQQLWHDKIDFVISEYGSKDKPEDITKWTILNALQKTL
ITWTFAVQVVLSAFIITKKEEVQQLWHDKIDFVISEYGSKDKPEDITKWTILNALQKTL
Sbjct: 65 ITWTFAVQVVLSAFIITKKEEVQQLWHDKIDFVISEYGSKDKPEDITKWTILNALQKTL

Query: 153 CCGQHNYTDWIKNKNKENSQVPCSTKSTLRKWFCDEPLNATYLEGCENKISAWYNVN
CCGQHNYTDWIKNKNKENSQVPCSTKSTLRKWFCDEPLNATYLEGCENKISAWYNVN
Sbjct: 125 CCGQHNYTDWIKNKNKENSQVPCSTKSTLRKWFCDEPLNATYLEGCENKISAWYNVN

Query: 213 LTLIGINFGLLTSEVFQVSLTVCFFKNIKNIHAEM 248
LTLIGINFGLLTSEVFQVSLTVCFFKNIKNIHAEM
Sbjct: 185 LTLIGINFGLLTSEVFQVSLTVCFFKNIKNIHAEM 220

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaCAABDaabr: 248 aa
>LEX 121 Seq id no 2
vs /tmp/fastaDAACDaabr library
searching /tmp/fastaDAACDaabr library

220 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 36, opt: 24, gap-pen: -12/ -2, width: 16
Scan time: 0.000

The best scores are: opt

gi|20553887|ref|XP_084868.4| similar to CD63 prot (220) 1497

>>gi|20553887|ref|XP_084868.4| similar to CD63 protein [(220 aa)

initn: 1497 init1: 1497 opt: 1497

Smith-Waterman score: 1497; 100.000% identity in 220 aa overlap (29-248:1-220)

	10	20	30	40	50	60
LEX	MLRNNKTIIIKYFLNLLINGAFLVLGLLFMGFGAWLLDRNNFLTAFDENNNHFIVPISQIL					
	::					
gi 205	MGFGAWLLDRNNFLTAFDENNNHFIVPISQIL					
		10	20	30		

	70	80	90	100	110	120
LEX	IGMGSSTVLFCLLGYIGIHNEIRWLLIVYAVLITWTFQVVLSAFIITKKEEVQQLWHD					
	::					
gi 205	IGMGSSTVLFCLLGYIGIHNEIRWLLIVYAVLITWTFQVVLSAFIITKKEEVQQLWHD					
	40	50	60	70	80	90

	130	140	150	160	170	180
LEX	KIDFVISEYGSKDKPEDITKWTILNALQKTLQCCGQHNYTDWIKNKNKENSQVPCSTK					
	::					
gi 205	KIDFVISEYGSKDKPEDITKWTILNALQKTLQCCGQHNYTDWIKNKNKENSQVPCSTK					
	100	110	120	130	140	150

	190	200	210	220	230	240
LEX	STLRKWFCDEPLNATYLEGCENKISAWYNVNVLTLLIGINFGLLTSEVFQVSLTVCFFKNI					
	::					
gi 205	STLRKWFCDEPLNATYLEGCENKISAWYNVNVLTLLIGINFGLLTSEVFQVSLTVCFFKNI					
	160	170	180	190	200	210

LEX	KNIIHAEM					
	::::::					
gi 205	KNIIHAEM					
	220					

248 residues in 1 query sequences

220 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Thu Aug 28 14:24:02 2003 done: Thu Aug 28 14:24:02 2003

Scan time: 0.000 Display time: 0.067

Compare Genomic Sequences

Function used was FASTA